

BLASTN 2.2.14 [May-07-2006]

RID: 1155134664-28197-77192316929.BLASTQ4

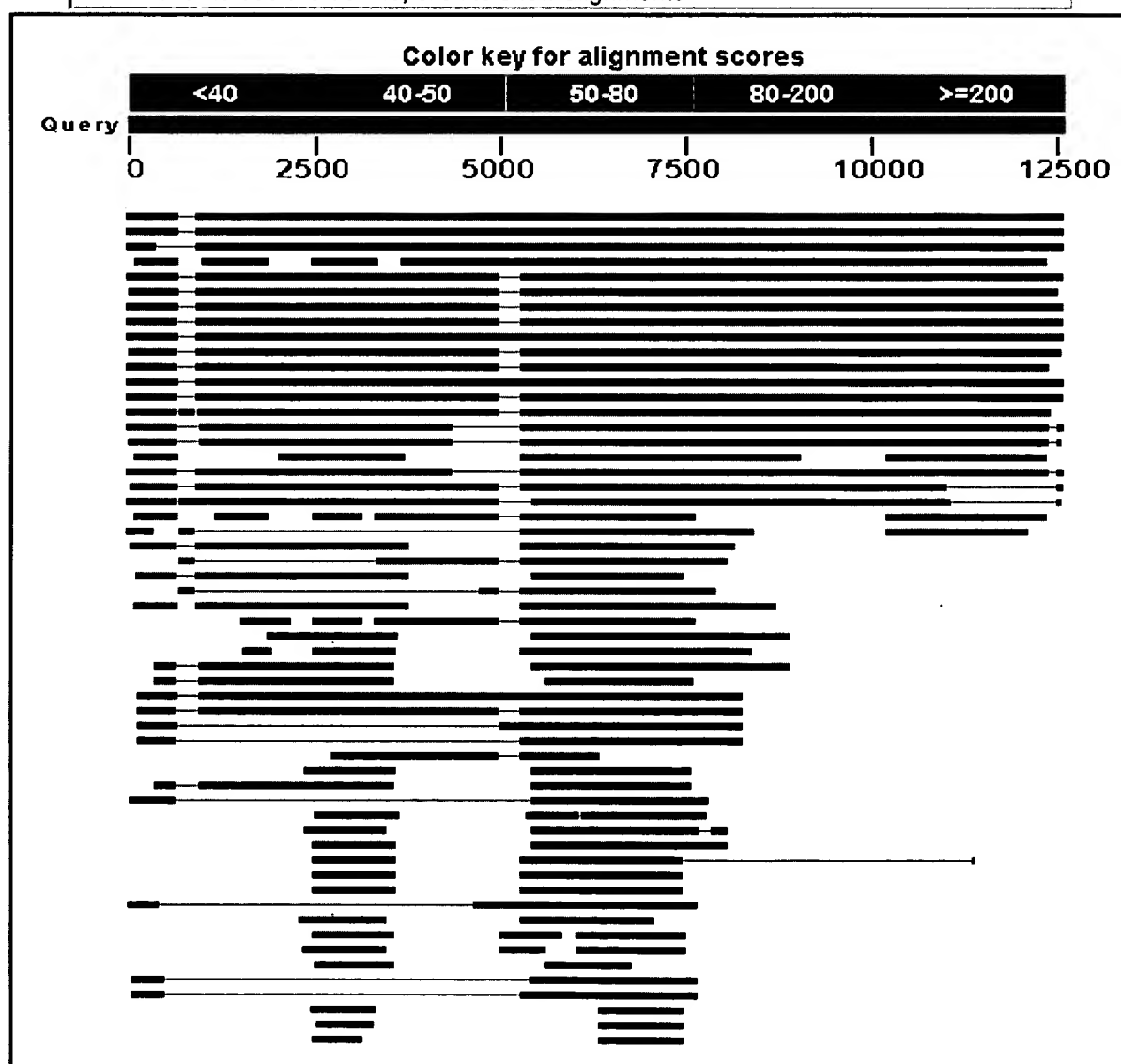
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
4,305,632 sequences; 17,928,720,935 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=12611

Distribution of 193 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



Sequences producing significant alignments:

	Score (Bits)	E Value	
gi 323205 gb M31182.1 BVDCG Bovine viral diarrhea virus 1-NADL,	2.140e+04	0.0	G
gi 7960753 emb AJ133738.1 BVI133738 Bovine viral diarrhea virus	2.132e+04	0.0	
gi 9049956 gb AF268278.1 AF268278 Pestivirus type 1, complete ge	2.131e+04	0.0	
gi 55724858 emb AJ781045.1 Bovine viral diarrhea virus parti...	1.573e+04	0.0	
gi 7960755 emb AJ133739.1 BVI133739 Bovine viral diarrhea vir...	1.333e+04	0.0	
gi 71727706 gb DQ088995.1 Bovine viral diarrhea virus 1 stra...	1.182e+04	0.0	
gi 289507 gb M96751.1 BVDPOLYPRO Bovine viral diarrhea virus ...	8981	0.0	
gi 3661565 gb AF091605.1 AF091605 Bovine viral diarrhea virus st	8937	0.0	
gi 28071149 dbj AB078951.1 Bovine viral diarrhea virus-1 gen...	8911	0.0	
gi 2789676 gb AF041040.1 AF041040 Pestivirus type 1 polyprotein	8841	0.0	
gi 2149468 gb U86600.1 PTU86600 Pestivirus type 1 noncytopathic	6423	0.0	
gi 28071151 dbj AB078952.1 Bovine viral diarrhea virus-1 gen...	6344	0.0	
gi 28071147 dbj AB078950.1 Bovine viral diarrhea virus-1 gen...	6274	0.0	
gi 2149466 gb U86599.1 PTU86599 Pestivirus type 1 cytopathic gen	5489	0.0	
gi 9836967 gb AF220247.1 AF220247 Bovine viral diarrhea virus-1,	5214	0.0	
gi 1518835 gb U63479.1 BVU63479 Bovine viral diarrhea virus 1...	5214	0.0	
gi 323222 gb M96641.1 BVDP12510A Bovine viral diarrhea virus ...	4745	0.0	
gi 37693100 emb AJ585412.1 Bovine viral diarrhea virus VEDEV...	4641	0.0	
gi 76781922 gb AF526381.3 Bovine viral diarrhea virus 1 strain	4501	0.0	
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gi 39725568 dbj AB111966.1 Bovine viral diarrhea virus 190cp...	3917	0.0	
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gi 3746673 gb AF078534.1 AF078534 Pestivirus type 1 strain Si...	3485	0.0	
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gi 323207 gb M62431.1 BVDCP1 Bovine viral diarrhea virus CP1 ...	3216	0.0	
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gi 289505 gb L12455.1 BVDSINGER Bovine viral diarrhea virus RNA	2636	0.0	
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gi 3885462 gb AF058699.1 AF058699 Bovine viral diarrhea virus...	2078	0.0	

Alignments

Get selected sequences

Select all

Deselect all

Distance tree of results

> **G** gi|323205|gb|M31182.1|BVDCG **G** Bovine viral diarrhea virus 1-NADL, complete genome
Length=12573

Score = 2.140e+04 bits (11589), Expect = 0.0
 Identities = 11670/11684 (99%), Gaps = 6/11684 (0%)
 Strand=Plus/Plus

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Query	8545	ATGGCCTTATTTGAAGCAGTCCAGACAATTGGTAACCCCTGAGACTAATATACCACCTG	8604
Sbjct	8510	8569
Query	8605	TATGGGGTTTACTACAAAGGTTGGGAGGCCAAGGAAGTATCTGAGAGGACAGCAGGCAGA	8664

Sbjct	8570	8629
Query	8665	AACTTATTCACATTGATAATGTTTGAAGCCTTCGAGTTATTAGGGATGGACTCACAAGGG	8724
Sbjct	8630	8689
Query	8725	AAAATAAGGAACCTGTCCGGAATTACATTTTGGATTTGATATACGGCCTACACAAGCAA	8784
Sbjct	8690	8749
Query	8785	ATCAACAGAGGGCTGAAGAAAATGGTACTGGGGTGGGCCCTGCACCCTTTAGTTGTGAC	8844
Sbjct	8750	8809
Query	8845	TGGACCCCTAGTGACGAGAGGATCAGATTGCCAACAGACAACTATTTGAGGGTAGAAACC	8904
Sbjct	8810	8869
Query	8905	AGGTGCCCATGTGGCTATGAGATGAAAGCTTTCAAAAATGTAGGTGGCAAACCTTACCAA	8964
Sbjct	8870	8929
Query	8965	GTGGAGGAGAGCGGGCCTTTCCTATGTAGAAACAGACCTGGTAGGGGACCAGTCAACTAC	9024
Sbjct	8930	8989
Query	9025	AGAGTCACCAAGTATTACGATGACAACCTCAGAGAGATAAAACCAGTAGCAAAGTTGGAA	9084
Sbjct	8990	9049
Query	9085	GGACAGGTAGAGCACTACTACAAAGGGGTACAGCAAAAATTGACTACAGTAAAGGAAAA	9144
Sbjct	9050	9109
Query	9145	ATGCTCTTGGCCACTGACAAGTGGGAGGTGGAACATGGTGTCTATAACCAGGTTAGCTAAG	9204
Sbjct	9110	9169
Query	9205	AGATATACTGGGGTCGGGTTCAATGGTGCATACTTAGGTGACGAGCCCAATCACCGTGCT	9264
Sbjct	9170	9229
Query	9265	CTAGTGGAGAGGGACTGTGCAACTATAACCAAAAACACAGTACAGTTTCTAAAAATGAAG	9324
Sbjct	9230	9289
Query	9325	AAGGGGTGTGCGTTCACCTATGACCTGACCATCTCCAATCTGACCAGGCTCATCGAACTA	9384
Sbjct	9290	9349
Query	9385	GTACACAGGAACAATCTTGAAGAGAAGGAAATACCCACCGCTACGGTCACCACATGGCTA	9444
Sbjct	9350	9409
Query	9445	GCTTACACCTTCGTGAATGAAGACGTAGGGACTATAAAACCAGTACTAGGAGAGAGAGTA	9504
Sbjct	9410	9469
Query	9505	ATCCCCGACCCTGTAGTTGATATCAATTTACAACCAGAGGTGCAAGTGGACACGTCAGAG	9564
Sbjct	9470	9529
Query	9565	GTTGGGATCACAATAATTGGAAGGGAAACCCTGATGACAACGGGAGTGACACCTGTCTTG	9624
Sbjct	9530	9589
Query	9625	GAAAAAGTAGAGCCTGACGCCAGCGACAACCAAACTCGGTGAAGATCGGGTTGGATGAG	9684
Sbjct	9590	9649
Query	9685	GGTAATTACCCAGGGCCTGGAATACAGACACATACTAACAGAAGAAATACACAACAGG	9744
Sbjct	9650	9709
Query	9745	GATGCGAGGCCCTTCATCATGATCCTGGGCTCAAGGAATTCATATCAAATAGGGCAAAG	9804
Sbjct	9710	9769
Query	9805	ACTGCTAGAAATATAAATCTGTACACAGGAAATGACCCAGGGAAATACGAGACTTGATG	9864
Sbjct	9770	9829
Query	9865	GCTGCAGGGCGCATGTTAGTAGTAGCACTGAGGGATGTGCGACCCTGAGCTGTCTGAAATG	9924
Sbjct	9830	9889

Query	9925	GTCGATTTCAAGGGGACTTTTTTAGATAGGGAGGCCCTGGAGGCTCTAAGTCTCGGGCAA	9984
Sbjct	9890	9949
Query	9985	CCTAAACCGAAGCAGGTTACCAAGGAAGCTGTTAGGAATTTGATAGAACAGAAAAAAGAT	10044
Sbjct	9950	10009
Query	10045	GTGGAGATCCCTAACTGGTTTGCATCAGATGACCCAGTATTTCTGGAAGTGGCCTTAAAA	10104
Sbjct	10010	10069
Query	10105	AATGATAAGTACTACTTAGTAGGAGATGTTGGAGAGCTAAAAGATCAAGCTAAAGCACTT	10164
Sbjct	10070	10129
Query	10165	GGGGCCACGGATCAGACAAGAATTATAAAGGAGGTAGGCTCAAGGACGTATGCCATGAAG	10224
Sbjct	10130	10189
Query	10225	CTATCTAGCTGGTTCC-CAAGGCATCAAACAAACAGATGAGTTTAACTCCACTGTTTGAG	10283
Sbjct	10190T.....	10249
Query	10284	GAATTGTTGCTACGGTGCCACCTGCAACTAAGAGCAATAAGGGGCACATGGCATCAGCT	10343
Sbjct	10250	10309
Query	10344	TACCAATTGGCACAGGGTAACTGGGAGCCCCTCGGTTGCGGGGTGCACCTAGGTACAATA	10403
Sbjct	10310	10369
Query	10404	CCAGCCAGAAGGGTGAAGATACACCCATATGAAGCTTACCTGAAGTTGAAAGATTTCAa	10463
Sbjct	10370	10429
Query	10464	gaagaagaagagaagaaACCTAGGGTTAAGGATACAGTAATAAGAGAGCACAAACAATGG	10523
Sbjct	10430	10489
Query	10524	ATACTTaaaaaaaTAAGGTTTCAAGGAAACCTCAACACCAAGAAAATGCTCAACCCAGGG	10583
Sbjct	10490	10549
Query	10584	AAACTATCTGAACAGTTGGACAGGGAGGGGCGCAAGAGGAACATCTACAACCACCAGATT	10643
Sbjct	10550	10609
Query	10644	GGTACTATAATGTCAAGTGCAGGCATAAGGCTGGAGAAATTGCCAATAGTGAGGGCCCAA	10703
Sbjct	10610	10669
Query	10704	ACCGACACCAAAACCTTTTCATGAGGCAATAAGAGATAAGATAGACAAGAGTGAAAACCGG	10763
Sbjct	10670	10729
Query	10764	CAAATCCAGAATTGCACAACAAATTGTTGGAGATTTTCCACACGATAGCCCAACCCACC	10823
Sbjct	10730	10789
Query	10824	CTGAAACACACCTACGGTGAGGTGACGTGGGAGCAACTTGAGGCGGGGGTAAATAGAAAG	10883
Sbjct	10790	10849
Query	10884	GGGGCAGCAGGCTTCCTGGAGAAGAAGAACATCGGAGAAGTATTGGATTGAGAAAAGCAC	10943
Sbjct	10850	10909
Query	10944	CTGGTAGAACAATTGGTCAGGGATCTGAAGGCCGGGAGAAAGATAAAATATTATGAACT	11003
Sbjct	10910	10969
Query	11004	GCAATACCAAAAAATGAGAAGAGAGATGTCAGTGATGACTGGCAGGCAGGGGACCTGGTG	11063
Sbjct	10970	11029
Query	11064	GTTGAGAAGAGGCCAAGAGTTATCCAATACCCTGAAGCCAAGACAAGGCTAGCCATCACT	11123
Sbjct	11030	11089
Query	11124	AAGGTCATGTATAACTGGGTGAAACAGCAGCCCGTTGTGATTCCAGGATATGAAGGAAAG	11183
Sbjct	11090	11149
Query	11184	ACCCCTTGTTCAACATCTTTGATAAAGTGAGAAAGGAATGGGACTCGTTCAATGAGCCA	11243
Sbjct	11150	11209

Query	11244	GTGGCCGTAAGTTTTTGACACCAAAGCCTGGGACACTCAAGTGACTAGTAAGGATCTGCAA	11303
Sbjct	11210	11269
Query	11304	CTTATTGGAGAAATCCAGAAATATTACTATAAGAAGGAGTGGCACAAGTTCATTGACACC	11363
Sbjct	11270	11329
Query	11364	ATCACCGACCACATGACAGAAGTACCAGTTATAACAGCAGATGGTGAAGTATATATAAGA	11423
Sbjct	11330	11389
Query	11424	AATGGGCAGAGAGGGAGCGGCCAGCCAGACACAAGTGCTGGCAACAGCATGTTAAATGTC	11483
Sbjct	11390	11449
Query	11484	CTGACAATGATGTACGGCTTCTGCGAAAGCACAGGGGTACCGTACAAGAGTTTCAACAGG	11543
Sbjct	11450	11509
Query	11544	GTGGCAAGGATCCACGTCTGTGGGGATGATGGCTTCTTAATAACTGAAAAAGGGTTAGGG	11603
Sbjct	11510	11569
Query	11604	CTGAAATTTGCTAACAAAGGGATGCAGATTCTTCATGAAGCAGGCAAACCTCAGAAGATA	11663
Sbjct	11570	11629
Query	11664	ACGGAAGGGGAAAAGATGAAAGTTGCCTATAGATTTGAGGATATAGAGTTCTGTTCTCAT	11723
Sbjct	11630	11689
Query	11724	ACCCAGTCCCTGTTAGGTGGTCCGACAACACCAGTAGTCACATGGCCGGGAGAGACACC	11783
Sbjct	11690	11749
Query	11784	GCTGTGATACTATCAAAGATGGCAACAAGATTGGATTCAAGTGGAGAGAGGGGTACCACA	11843
Sbjct	11750	11809
Query	11844	GCATATGAAAAAGCGGTAGCCTTCAGTTTCTTGCTGATGTATTCCTGGAACCCGCTTGTT	11903
Sbjct	11810	11869
Query	11904	AGGAGGATTTGCCTGTTGGTCCTTTCGCAACAGCCAGAGACAGACCCATCAAAACATGCC	11963
Sbjct	11870	11929
Query	11964	ACTTATTATTACAAAGGTGATCCAATAGGGGCCTATAAAGATGTAATAGGTCGGAATCTA	12023
Sbjct	11930	11989
Query	12024	AGTGAAGTGAAGAGAACAGGCTTTGAGAAATTGGCAAATCTAAACCTAAGCCTGTCCACG	12083
Sbjct	11990	12049
Query	12084	TTGGGGGTCTGGACTAAGCACACAAGCAAAAGAATAATTTCAGGACTGTGTTGCCATTGGG	12143
Sbjct	12050	12109
Query	12144	AAAGAAGAGGGCAACTGGCTAGTTAAGCCCGACAGGCTGATATCCAGCAAAACTGGCCAC	12203
Sbjct	12110	12169
Query	12204	TTATACATACCTGATAAAGGCTTTACATTACAAGGAAAGCATTATGAGCAACTGCAGCTA	12263
Sbjct	12170	12229
Query	12264	AGAACAGAGACAAACCCGGTCATGGGG- TTGGGACTGAGAGATACAAGTTAGGTCCATA	12322
Sbjct	12230G.....	12289
Query	12323	GTCAATCTGCTGCTGAGAAGGTTGAAAATTCTGCTCATGACGGCCGTCGGCGTCAGCAGC	12382
Sbjct	12290	12349
Query	12383	TGAGACAAAATGTATATATTGTAAATAAATTAATCCATGTACATAGTGTATATAAATATA	12442
Sbjct	12350	12409
Query	12443	GTTGGGACCGTCCACCTCAAGAAGACGACACGCCCAACACGCACAGCTAAACAGTAGTCA	12502
Sbjct	12410	12469
Query	12503	AGATTATCTACCTCAAGATAACACTACATTTAATGCACACAGCACTTTAGCTGTATGAGG	12562

Sbjct 12470 12529

Query 12563 ATACGCCCCGACGTCTATAGTTGGACTAGGGAAGACCTCTAACAG 12606

Sbjct 12530 12573

Score = 1284 bits (695), Expect = 0.0

Identities = 695/695 (100%), Gaps = 0/695 (0%)

Strand=Plus/Plus

Query 1 GTATACGAGAATTAGAAAAGGCACTCGTATACGTATTGGGCAATTAAAAATAATAATTAG 60

Sbjct 1 60

Query 61 GCCTAGGGAACAAATCCCTCTCAGCGAAGGCCGAAAAGAGGCTAGCCATGCCCTTAGTAG 120

Sbjct 61 120

Query 121 GACTAGCATAATGAGGGGGGTAGCAACAGTGGTGAGTTCGTTGGATGGCTTAAGCCCTGA 180

Sbjct 121 180

Query 181 GTACAGGGTAGTCGTCAGTGGTTCGACGCCTTGAATAAAGGTCTCGAGATGCCACGTGG 240

Sbjct 181 240

Query 241 ACGAGGGCATGCCCCAAGCACATCTTAACCTGAGCGGGGGTCGCCCAGGTAAAAGCAGTT 300

Sbjct 241 300

Query 301 TTAACCGACTGTTACGAATACAGCCTGATAGGGTGCTGCAGAGGCCCACTGTATTGCTAC 360

Sbjct 301 360

Query 361 TAAAAATCTCTGCTGTACATGGCACATGGAGTTGATCACAAATGAACTTTTATACAAAAC 420

Sbjct 361 420

Query 421 ATACAAACAAAACCCGTCGGGGTGGAGGAACCTGTTTATGATCAGGCAGGTGATCCCTT 480

Sbjct 421 480

Query 481 ATTTGGTGAAAGGGGAGCAGTCCACCCTCAATCGACGCTAAAGCTCCCACACAAGAGAGG 540

Sbjct 481 540

Query 541 GGAACGCGATGTTCCAACCAACTTGGCATCCTTACCAAAAAGAGGTGACTGCAGGTGCGG 600

Sbjct 541 600

Query 601 TAATAGCAGAGGACCTGTGAGCGGGATCTACCTGAAGCCAGGGCCACTATTTTACCAGGA 660

Sbjct 601 660

Query 661 CTATAAAGGTCCCGTCTATCACAGGGCCCCGCTGG 695

Sbjct 661 695

> [gi|7960753|emb|AJ133738.1|BVI133738](#) **D** Bovine viral diarrhea virus complete RNA genome, isolate
Length=12578

Score = 2.132e+04 bits (11546), Expect = 0.0

Identities = 11660/11690 (99%), Gaps = 8/11690 (0%)

Strand=Plus/Plus

Query 929 TCAGACACGAAAGAAGAGGGAGCAACAAAAAGAAAACACAGAAACCCGACAGACTAGAA 988

Sbjct 890 949

Query 989 AGGGGGAAAATGAAAATAGTGCCCAAGAATCTGAAAAGACAGCAAACTAAACCTCCG 1048

Sbjct 950 1009

Query 1049 GATGCTACAATAGTGGTGAAGGAGTCAAATACCAGGTGAGGAAGAAGGGAAAAACCAAG 1108

Sbjct 1010 1069

Query 1109 AGTAAAAACACTCAGGACGGCTTGTACCATAACAAAAACAAACCTCAGGAATCACGCAAG 1168

Sbjct 1070 1129

Query	1169	AAACTGGAAAAAGCATTGTTGGCGTGGGCAATAATAGCTATAGTTTTGTTTCAAGTTACA	1228
Sbjct	1130	1189
Query	1229	ATGGGAGAAAACATAACACAGTGAACCTACAAGATAATGGGACGGAAGGGATACAACGG	1288
Sbjct	1190	1249
Query	1289	GCAATGTTCCAAAGGGGTGTGAATAGAAGTTTACATGGAATCTGGCCAGAGAAAATCTGT	1348
Sbjct	1250	1309
Query	1349	ACTGGCGTCCCTTCCCATCTAGCCACCGATATAGAACTAAAAACAATTCATGGTATGATG	1408
Sbjct	1310T.....	1369
Query	1409	GATGCAAGTGAGAAGACCAACTACACGTGTTGCAGACTTCAACGCCATGAGTGGAACAAG	1468
Sbjct	1370	1429
Query	1469	CATGGTTGGTGCAACTGGTACAATATTGAACCCTGGATTCTAGTCATGAATAGAACCCAA	1528
Sbjct	1430	1489
Query	1529	GCCAATCTCACTGAGGGACAACCACCAAGGGAGTGCGCAGTCACTTGTAGGTATGATAGG	1588
Sbjct	1490	1549
Query	1589	GCTAGTGACTTAAACGTGGTAACACAAGCTAGAGATAGCCCCACACCCTTAACAGGTTGC	1648
Sbjct	1550	1609
Query	1649	AAGAAAGGAAAGAACTTCTCCTTTGCAGGCATATTGATGCGGGGCCCTGCAACTTTGAA	1708
Sbjct	1610	1669
Query	1709	ATAGCTGCAAGTGATGTATTATTCAAAGAACATGAACGCATTAGTATGTTCCAGGATACT	1768
Sbjct	1670	1729
Query	1769	ACTCTTTACCTTGTTGACGGGTTGACCAACTCCTTAGAAGGTGCCAGACAAGGAACCGCT	1828
Sbjct	1730	1789
Query	1829	AAACTGACAACCTGGTTAGGCAAGCAGCTCGGGATACTAGGAAAAAAGTTGGAAAACAAG	1888
Sbjct	1790	1849
Query	1889	AGTAAGACGTGGTTTGGAGCATACGCTGCTTCCCCTTACTGTGATGTGATCGCAAAATT	1948
Sbjct	1850	1909
Query	1949	GGCTACATATGGTATACAAAAAATTGCACCCCTGCCTGCTTACCCAAGAACACAAAAATT	2008
Sbjct	1910	1969
Query	2009	GTCGGCCCTGGGAAATTTGACACCAATGCAGAGGACGGCA-GATATTACATGAGATGGGG	2067
Sbjct	1970A.....	2029
Query	2068	GGTCACTTGTGCGAGGTACTACTACTTTCTTTAGTGGTGTGTCCGACTTCGCACCGGAA	2127
Sbjct	2030	2089
Query	2128	ACAGCTAGTGTAATGTACCTAATCCTACATTTTTCCATCCCACAAAGTCACGTTGATGTA	2187
Sbjct	2090	2149
Query	2188	ATGGATTGTGATAAGACCCAGTTGAACCTCACAGTGGAGCTGACAACAGCTGAAGTAATA	2247
Sbjct	2150T.....	2209
Query	2248	CCAGGGTCGGTCTGGAATCTAGGCAAATATGTATGTATAAGACCAAATTGGTGGCCTTAT	2307
Sbjct	2210	..T..A..A.....C.....GG.....	2269
Query	2308	GAGACAAGTGTAGTGTGGCATTGTAAGAGGTGAGCCAGGTGGTGAAGTTAGTGTTGAGG	2367
Sbjct	2270G.....	2329
Query	2368	GCACTCAGAGATTTAACACGCATTTGGAACGCTGCAACAAGTACTGCTTTTTTAGTATGC	2427
Sbjct	2330G.....C...A.....	2389
Query	2428	CTTGTTAAGATAGTCAGGGGCCAGATGGTACAGGGCATTCTGTGGCTACTATTGATAACA	2487

Sbjct	2390C.....	2449
Query	2488	GGGGTACAAGGGCACTTGGATTGCAAACCTGAATTCTCGTATGCCATAGCAAAGGACGAA	2547
Sbjct	2450	2509
Query	2548	AGAATTGGTCAACTGGGGGCTGAAGGCCTTACCACCACCTTGAAGGAATACTCACCTGGA	2607
Sbjct	2510	2569
Query	2608	ATGAAGCTGGAAGACACAATGGTCATTGCTTGGTGCGAAGATGGGAAGTTAATGTACCTC	2667
Sbjct	2570	2629
Query	2668	CAAAGATGCACGAGAGAAAACCAGATATCTCGCAATCTTGCATACAAGAGCCTTGCCGACC	2727
Sbjct	2630	2689
Query	2728	AGTGTGGTATTCAAAAACTCTTTGATGGGCGAAAGCAAGAGGATGTAGTCGAAATGAAC	2787
Sbjct	2690	2749
Query	2788	GACAACTTTGAATTTGGACTCTGCCCATGTGATGCCAAACCCATAGTAAGAGGGAAGTTC	2847
Sbjct	2750	2809
Query	2848	AATACAACGCTGCTGAACGGACCGGCCTTCCAGATGGTATGCCCCATAGGATGGACAGGG	2907
Sbjct	2810	2869
Query	2908	ACTGTAAGCTGTACGTCATTCAATATGGACACCTTAGCCACAACCTGTGGTACGGACATAT	2967
Sbjct	2870	2929
Query	2968	AGAAGGTCTAAACCATTCCCTCATAGGCAAGGCTGTATCACCCAAAAGAATCTGGGGGAG	3027
Sbjct	2930	2989
Query	3028	GATCTCCATAACTGCATCCTTGGAGGAAATTGGACTTGTGTGCCTGGAGACCAACTACTA	3087
Sbjct	2990	3049
Query	3088	TACAAAGGGGGCTCTATTGAATCTTGCAAGTGGTGTGGCTATCAATTTAAAGAGAGTGAG	3147
Sbjct	3050	3109
Query	3148	GGACTACCACACTACCCCATTGGCAAGTGTAATTTGGAGAACGAGACTGGTTACAGGCTA	3207
Sbjct	3110	3169
Query	3208	GTAGACAGTACCTCTTGCAATAGAGAAGGTGTGGCCATAGTACCACAAGGGACATTAAAG	3267
Sbjct	3170	3229
Query	3268	TGCAAGATAGGAAAAACAACGTACAGGTCATAGCTATGGATACCAAACCTCGGACCTATG	3327
Sbjct	3230	3289
Query	3328	CCTTGCAGACCATATGAAATCATATCAAGTGAGGGGCCTGTAGAAAAGACAGCGTGTACT	3387
Sbjct	3290	3349
Query	3388	TTCAACTACACTAAGACATTAAAAATAAGTATTTTGAGCCCAGAGACAGCTACTTTCAG	3447
Sbjct	3350	3409
Query	3448	CAATACATGCTAAAAGGAGAGTATCAATACTGGTTTGACCTGGAGGTGACTGACCATCAC	3507
Sbjct	3410	3469
Query	3508	CGGGATTACTTCGCTGAGTCCATATTAGTGGTGGTAGTAGCCCTCTTGGGTGGCAGATAT	3567
Sbjct	3470	3529
Query	3568	GTACTTTGGTTACTGGTTACATACATGGTCTTATCAGAACAGAAGGCCTTAGGGATTTCAG	3627
Sbjct	3530	3589
Query	3628	TATGGATCAGGGGAAGTGGTGATGATGGGCAACTTGCTAACCATAACAATATTGAAGTG	3687
Sbjct	3590	3649
Query	3688	GTGACATACTTCTTGCTGCTGTACCTACTGCTGAGGGAGGAGAGCGTAAAGAAGTGGGTC	3747
Sbjct	3650	3709

Query	3748	TTACTCTTATACCACATCTTAGTGGTACACCCAATCAAATCTGTAATTGTGATCCTACTG	3807
Sbjct	3710	3769
Query	3808	ATGATTGGGGATGTGGTAAAGGCCGATTTCAGGGGGCCAAGAGTACTTGGGGAAAATAGAC	3867
Sbjct	3770	3829
Query	3868	CTCTGTTTTACAACAGTAGTACTAATCGTCATAGGTTTAAATCATAGCCAGGCGTGACCCA	3927
Sbjct	3830	3889
Query	3928	ACTATAGTGCCACTGGTAACAATAATGGCAGCACTGAGGGTCACTGAACTGACCCACCAG	3987
Sbjct	3890	3949
Query	3988	CCTGGAGTTGACATCGCTGTGGCGGTCATGACTATAACCCTACTGATGGTTAGCTATGTG	4047
Sbjct	3950	4009
Query	4048	ACAGATTATTTTAGATATAAAAAATGGTTACAGTGCATTCTCAGCCTGG-ATCTGGGGTG	4106
Sbjct	4010T.....	4069
Query	4107	TTCTTGATAAGAAGCCTAATATACCTAGGTAGAATCGAGATGCCAGAGGTAACATCCCA	4166
Sbjct	4070	4129
Query	4167	AACTGGAGACCACTAACTTTAATACTATTATATTTGATCTCAACAACAATTGTAACGAGG	4226
Sbjct	4130	4189
Query	4227	TGGAAGGTTGACGTGGCTGGCCTATTGTTGCAATGTGTGCCTATCTTATTGCTGGTCACA	4286
Sbjct	4190	4249
Query	4287	ACCTTGTGGGCCGACTTCTTAACCCTAATACTGATCCTGCCTACCTATGAATTGGTTAAA	4346
Sbjct	4250	4309
Query	4347	TTATACTATCTGAAAACGTGTTAGGACTGATATAGAAAGAAGTTGGCTAGGGGGGATAGAC	4406
Sbjct	4310	4369
Query	4407	TATACAAGAGTTGACTCCATCTACGACGTTGATGAGAGTGGAGAGGGCGTATATCTTTTT	4466
Sbjct	4370	4429
Query	4467	CCATCAAGGCAGAAAGCACAGGGGAATTTTTCTATACTCTTGCCCCTTATCAAAGCAACA	4526
Sbjct	4430	4489
Query	4527	CTGATAAGTTGCGTCAGCAGTAAATGGCAGCTAATATACATGAGTTACTTAACTTTGGAC	4586
Sbjct	4490	4549
Query	4587	TTTATGTACTACATGCACAGGAAAGTTATAGAAGAGATCTCAGGAGGTACCAACATAATA	4646
Sbjct	4550	4609
Query	4647	TCCAGGTTAGTGGCAGCACTCATAGAGCTGAACTGGTCCATGGAAGAAGAGGAGAGCAAA	4706
Sbjct	4610	4669
Query	4707	GGCTTAAAGAAGTTTTATCTATTGTCTGGAAGGTTGAGAAACCTAATAATAAACATAAG	4766
Sbjct	4670	4729
Query	4767	GTAAGGAATGAGACCGTGGCTTCTTGGTACGGGGAGGAGGAAGTCTACGGTATGCCAAAG	4826
Sbjct	4730	4789
Query	4827	ATCATGACTATAATCAAGGCCAGTACACTGAGTAAGAGCAGGCACTGCATAATATGCACT	4886
Sbjct	4790	4849
Query	4887	GTATGTGAGGGCCGAGAGTGGAAAGGTGGCACCTGCCCCAAATGTGGACGCCATGGGAAG	4946
Sbjct	4850	4909
Query	4947	CCGATAACGTGTGGGATGTGCTAGCAGATTTCTGAAGAAAGACACTATAAAAGAATCTTT	5006
Sbjct	4910	4969
Query	5007	ATAAGGGAAGGCAACTTTGAGGGTATGTGCAGCCGATGCCAGGGAAAGCATAGGAGGTTT	5066
Sbjct	4970	5029

Query	5067	GAAATGGACCGGGAACCTAAGAGTGCCAGATACTGTGCTGAGTGTAATAGGCTGCATCCT	5126
Sbjct	5030	5089
Query	5127	GCTGAGGAAGGTGACTTTTGGGCAGAGTCGAGCATGTTGGGCCTCAAATCACCTACTTT	5186
Sbjct	5090	5149
Query	5187	GCGCTGATGGATGGAAAGGTGTATGATATCACAGAGTGGGCTGGATGCCAGCGTGTGGGA	5246
Sbjct	5150	5209
Query	5247	ATCTCCCCAGATACCCACAGAGTCCCTTGTCACATCTCATTTGGTTCACGGATGCCTTTC	5306
Sbjct	5210	5269
Query	5307	AGGCAGGAATACAATGGCTTTGTACAATATACCGCTAGGGGGCAACTATTTCTGAGAAAC	5366
Sbjct	5270	5329
Query	5367	TTGCCCGTACTGGCAACTAAAGTAAAAATGCTCATGGTAGGCAACCTTGGAGAAGAAATT	5426
Sbjct	5330	5389
Query	5427	GGTAATCTGGAACATCTTGGGTGGATCCTAAGGGGGCCTGCCGTGTGTAAGAAGATCACA	5486
Sbjct	5390	5449
Query	5487	GAGCACGAAAAATGCCACATTAATATACTGGATAAACTAACCGCATTTTTTCGGGATCATG	5546
Sbjct	5450	5509
Query	5547	CCAAGGGGGACTACACCCAGAGCCCCGGTGAGGTTCCCTACGAGCTTACTAAAAGTGAGG	5606
Sbjct	5510	5569
Query	5607	AGGGGTCTGGGAGACTGGCTGGGCTTACACACACCAAGGCGGGATAAGTTCAGTCGACCAT	5666
Sbjct	5570	5629
Query	5667	GTAACCGCCGGAAAAGATCTACTGGTCTGTGACAGCATGGGACGAACTAGAGTGGTTTGC	5726
Sbjct	5630	5689
Query	5727	CAAAGCAACAACAGGTTGACCGATGAGACAGAGTATGGCGTCAAGACTGACTCAGGGTGC	5786
Sbjct	5690	5749
Query	5787	CCAGACGGTGCCAGATGTTATGTGTAAATCCAGAGGCCGTTAACATATCAGGATCCAAA	5846
Sbjct	5750	5809
Query	5847	GGGGCAGTCGTTACCTCCAAAAGACAGGTGGAGAATTACGTGTGTACCCGCATCAGGC	5906
Sbjct	5810	5869
Query	5907	ACACCGGCTTTCTTCGACCTAAAAAACTTGAAAGGATGGTCAGGCTTGCCTATATTTGAA	5966
Sbjct	5870	5929
Query	5967	GCCTCCAGCGGGAGGGTGGTTGGCAGAGTCAAAGTAGGGAAGAATGAAGAGTCTAAACCT	6026
Sbjct	5930	5989
Query	6027	ACAAAAATAATGAGTGGAATCCAGACCGTCTCAAAAAACACAGCAGACCTGACCGAGATG	6086
Sbjct	5990	6049
Query	6087	GTCAAGAAGATAACCAGCATGAACAGGGGAGACTTCAAGCAGATTACTTTGGCAACAGGG	6146
Sbjct	6050	6109
Query	6147	-CAGGCAAAACCACAGAACTCCCAAAAGCAGTTATAGAGGAGATAGGAAGACACAAGAGA	6205
Sbjct	6110	G.....	6169
Query	6206	GTATTAGTTCTTATACCATTAAGGGCAGCGGCAGAGTCAGTCTACCAGTATATGAGATTG	6265
Sbjct	6170	6229
Query	6266	AAACACCCAAGCATCTCTTTTAACCTAAGGATAGGGGACATGAAAGAGGGGGACATGGCA	6325
Sbjct	6230	6289
Query	6326	ACCGGGATAACCTATGCATCATACGGGTACTTCTGCCAAATGCCTCAACCAAAGCTCAGA	6385

Sbjct	6290	6349
Query	6386	GCTGCTATGGTAGAATACTCATACATATTCTTAGATGAATACCATTGTGCCACTCCTGAA	6445
Sbjct	6350	6409
Query	6446	CAACTGGCAATTATCGGGAAGATCCACAGATTTTCAGAGAGTATAAGGGTTGTCGCCATG	6505
Sbjct	6410	6469
Query	6506	ACTGCCACGCCAGCAGGGTCGGTGACCACAACAGGTCAAAGCACCCAATAGAGGAATTC	6565
Sbjct	6470	6529
Query	6566	ATAGCCCCCGAGGTAATGAAAGGGGAGGATCTTGGTAGTCAGTTCCTTGATATAGCAGGG	6625
Sbjct	6530	6589
Query	6626	TTAAAAATACCAGTGGATGAGATGAAAGGCAATATGTTGGTTTTTGTACCAACGAGAAAC	6685
Sbjct	6590	6649
Query	6686	ATGGCAGTAGAGGTAGCAAAGAAGCTAAAAGCTAAGGGCTATAACTCTGGATACTATTAC	6745
Sbjct	6650	6709
Query	6746	AGTGGAGAGGATCCAGCCAATCTGAGAGTTGTGACATCACAATCCCCCTATGTAATCGTG	6805
Sbjct	6710	6769
Query	6806	GCTACAAATGCTATTGAATCAGGAGTGACACTACCAGATTTGGACACGGTTATAGACACG	6865
Sbjct	6770	6829
Query	6866	GGGTTGAAATGTGAAAAGAGGGTGAGGGTATCATCAAAGATACCCTTCATCGTAACAGGC	6925
Sbjct	6830	6889
Query	6926	CTTAAGAGGATGGCCGTGACTGTGGGTGAGCAGGCGCAGCGTAGGGGCAGAGTAGGTAGA	6985
Sbjct	6890	6949
Query	6986	GTGAAACCCGGGAGGTATTATAGGAGCCAGGAAACAGCAACAGGGTCAAAGGACTACCAC	7045
Sbjct	6950T....	7009
Query	7046	TATGACCTCTTGCAGGCACAAAGATACGGGATTGAGGATGGAATCAACGTGACGAAATCC	7105
Sbjct	7010	7069
Query	7106	TTTAGGGAGATGAATTACGATTGGAGCCTATACGAGGAGGACAGCCTACTAATAACCCAG	7165
Sbjct	7070	7129
Query	7166	CTGGAAATACTAAATAATCTACTCATCTCAGAAGACTTGCCAGCCGCTGTTAAGAACATA	7225
Sbjct	7130	7189
Query	7226	ATGGCCAGGACTGATCACCCAGAGCCAATCCAACCTGCATACAACAGCTATGAAGTCCAG	7285
Sbjct	7190	7249
Query	7286	GTCCCGGTCTTATTCCTAAAAATAAGGAATGGAGAAGTCACAGACACCTACGAAAATTAC	7345
Sbjct	7250G.....	7309
Query	7346	TCGTTTCTAAATGCCAGAAAGTTAGGGGAGGATGTGCCCGTGTATATCTACGCTACTGAA	7405
Sbjct	7310	7369
Query	7406	GATGAGGATCTGGCAGTTGACCTCTTAGGGCTAGACTGGCCTGATCCTGGGAACCAGCAG	7465
Sbjct	7370	7429
Query	7466	GTAGTGGAGACTGGTAAAGCACTGAAGCAAGTGACCGGGTTGTCCTCGGCTGAAAATGCC	7525
Sbjct	7430	7489
Query	7526	CTACTAGTGGCTTTATTTGGGTATGTGGGTTACCAGGCTCTCTCAAAGAGGCATGTCCCA	7585
Sbjct	7490	7549
Query	7586	ATGATAACAGACATATATACCATCGAGGACCAGAGACTAGAAGACACCACCCACCTCCAG	7645
Sbjct	7550	7609

Query	7646	TATGCACCCAACGCCATAAAAACCGATGGGACAGAGACTGAACTGAAAGAACTGGCGTCG	7705
Sbjct	7610	7669
Query	7706	GGTGACGTGGAAAAATCATGGGAGCCATTTTCTAGATTATGCAGCTGGGGGACTGGAGTTT	7765
Sbjct	7670	7729
Query	7766	GTTAAATCCCAAGCAGAAAAGATAAAAACAGCTCCTTTGTTTAAAGAAAACGCAGAAGCC	7825
Sbjct	7730	7789
Query	7826	GCAAAAGGGTATGTCCAAAAATTCATTGACTCATTAATTGAAAATAAAGAAGAAATAATC	7885
Sbjct	7790	7849
Query	7886	AGATATGGTTTGTGGGGAACACACACAGCACTATACAAAAGCATAGCTGCAAGACTGGGG	7945
Sbjct	7850	7909
Query	7946	CATGAAACAGCGTTTGGCCACACTAGTGTTAAAGTGGCTAGCTTTTGGAGGGGAATCAGTG	8005
Sbjct	7910	7969
Query	8006	TCAGACCACGTCAAGCAGGCGGCAGTTGATTTAGTGGTCTATTATGTGATGAATAAGCCT	8065
Sbjct	7970	8029
Query	8066	TCCTTCCCAGGTGACTCCGAGACACAGCAAGAAGGGAGGCGATTGTCGCAAGCCTGTTC	8125
Sbjct	8030	8089
Query	8126	ATCTCCGCACTGGCAACCTACACATACAAAACCTTGAATTACCACAATCTCTCTAAAGTG	8185
Sbjct	8090	8149
Query	8186	GTGGAAC-AGCCCTGGCTTACCTCCCCTATGCTACCAGCGCATTAAAAATGTTACCCCA	8244
Sbjct	8150C.....	8209
Query	8245	ACGCGGCTGGAGAGCGTGGTGATACTGAGCACCACGATATATAAAACATACCTCTCTATA	8304
Sbjct	8210	8269
Query	8305	AGGAAGGGGAAGAGTGATGGATTGCTGGGTACGGGGATAAGTGCAGCCATGGAAATCCTG	8364
Sbjct	8270	8329
Query	8365	TCACAAAACCCAGTATCGGTAGGTATATCTGTGATGTTGGGGGTAGGGGCAATCGCTGCG	8424
Sbjct	8330	8389
Query	8425	CACAACGCTATTGAGTCCAGTGAACAGAAAAGGACCCTACTTATGAAGGTGTTTGTAAAG	8484
Sbjct	8390	8449
Query	8485	AACTTCTTGGATCAGGCTGCAACAGATGAGCTGGTAAAAGAAAACCCAGAAAAAATTATA	8544
Sbjct	8450	8509
Query	8545	ATGGCCTTATTTGAAGCAGTCCAGACAATTGGTAACCCCTGAGACTAATATACCACCTG	8604
Sbjct	8510	8569
Query	8605	TATGGGGTTTACTACAAAGGTTGGGAGGCCAAGGAACTATCTGAGAGGACAGCAGGCAGA	8664
Sbjct	8570	8629
Query	8665	AACTTATTCACATTGATAATGTTTGAAGCCTTCGAGTTATTAGGGATGGACTCACAAGGG	8724
Sbjct	8630	8689
Query	8725	AAAATAAGGAACCTGTCCGGAATTACATTTTGGATTTGATATACGGCCTACACAAGCAA	8784
Sbjct	8690	8749
Query	8785	ATCAACAGAGGGCTGAAGAAAATGGTACTGGGGTGGGCCCTGCACCCTTTAGTTGTGAC	8844
Sbjct	8750	8809
Query	8845	TGGACCCCTAGTGACGAGAGGATCAGATTGCCAACAGACAACCTATTTGAGGGTAGAAACC	8904
Sbjct	8810	8869
Query	8905	AGGTGCCCATGTGGCTATGAGATGAAAGCTTTCAAAAATGTAGGTGGCAAACCTTACCAA	8964
Sbjct	8870	8929

Query	8965	GTGGAGGAGAGCGGGCCTTTCTCTATGTAGAAACAGACCTGGTAGGGGACCAGTCAACTAC	9024
Sbjct	8930	8989
Query	9025	AGAGTCACCAAGTATTACGATGACAACCTCAGAGAGATAAAACCAGTAGCAAAGTTGGAA	9084
Sbjct	8990	9049
Query	9085	GGACAGGTAGAGCACTACTACAAAGGGGTACAGCAAAAATTGACTACAGTAAAGGAAAA	9144
Sbjct	9050	9109
Query	9145	ATGCTCTTGGCCACTGACAAGTGGGAGGTGGAACATGGTGTCTATAACCAGGTTAGCTAAG	9204
Sbjct	9110	9169
Query	9205	AGATATACTGGGGTCGGGTTCAATGGTGCATACTTAGGTGACGAGCCCAATCACCGTGCT	9264
Sbjct	9170	9229
Query	9265	CTAGTGGAGAGGGACTGTGCAACTATAACCAAAAACACAGTACAGTTTCTAAAAATGAAG	9324
Sbjct	9230	9289
Query	9325	AAGGGGTGTGCGTTCACCTATGACCTGACCATCTCCAATCTGACCAGGCTCATCGAACTA	9384
Sbjct	9290	9349
Query	9385	GTACACAGGAACAATCTTGAAGAGAAGGAAATACCCACCGCTACGGTCACCACATGGCTA	9444
Sbjct	9350	9409
Query	9445	GCTTACACCTTCGTGAATGAAGACGTAGGGACTATAAAACCAGTACTAGGAGAGAGAGTA	9504
Sbjct	9410	9469
Query	9505	ATCCCCGACCCTGTAGTTGATATCAATTTACAACCAGAGGTGCAAGTGGACACGTCAGAG	9564
Sbjct	9470	9529
Query	9565	GTTGGGATCACAATAATTGGAAGGGAAACCCTGATGACAACGGGAGTGACACCTGTCTTG	9624
Sbjct	9530	9589
Query	9625	GAAAAAGTAGAGCCTGACGCCAGCGACAACCAAACTCGGTGAAGATCGGGTTGGATGAG	9684
Sbjct	9590	9649
Query	9685	GGTAATTACCCAGGGCCTGGAATACAGACACATACACTAACAGAAGAAATACACAACAGG	9744
Sbjct	9650	9709
Query	9745	GATGCGAGGCCCTTCATCATGATCCTGGGCTCAAGGAATTCATATCAAATAGGGCAAAG	9804
Sbjct	9710	9769
Query	9805	ACTGCTAGAAATATAAATCTGTACACAGGAAATGACCCAGGGAAATACGAGACTTGATG	9864
Sbjct	9770	9829
Query	9865	GCTGCAGGGCGCATGTTAGTAGTAGCACTGAGGGATGTCGACCCTGAGCTGTCTGAAATG	9924
Sbjct	9830	9889
Query	9925	GTCGATTTCAAGGGGACTTTTTTAGATAGGGAGGCCCTGGAGGCTCTAAGTCTCGGGCAA	9984
Sbjct	9890	9949
Query	9985	CCTAAACCGAAGCAGGTTACCAAGGAAGCTGTTAGGAATTTGATAGAACAGAAAAAGAT	10044
Sbjct	9950	10009
Query	10045	GTGGAGATCCCTAACTGGTTTGCATCAGATGACCCAGTATTTCTGGAAGTGGCCTTAAAA	10104
Sbjct	10010	10069
Query	10105	AATGATAAGTACTACTTAGTAGGAGATGTTGGAGAGCTAAAAGATCAAGCTAAAGCACTT	10164
Sbjct	10070G.....	10129
Query	10165	GGGGCCACGGATCAGACAAGAATTATAAAGGAGGTAGGCTCAAGGACGTATGCCATGAAG	10224
Sbjct	10130	10189
Query	10225	CTATCTAGCTGGTTCC-CAAGGCATCAAACAAACAGATGAGTTTAACTCCACTGTTTGAG	10283

Sbjct	10190T.C.....	10249
Query	10284	GAATTGTTGCTACGGTGCCACCTGCAACTAAGAGCAATAAGGGGCACATGGCATCAGCT	10343
Sbjct	10250	10309
Query	10344	TACCAATTGGCACAGGGTAACTGGGAGCCCCTCGGTTGCGGGGTGCACCTAGGTACAATA	10403
Sbjct	10310	10369
Query	10404	CCAGCCAGAAGGGTGAAGATACACCCATATGAAGCTTACCTGAAGTTGAAAGATTTCAa	10463
Sbjct	10370	10429
Query	10464	gaagaagaagagaagaaACCTAGGGTTAAGGATACAGTAATAAGAGAGCACAAACAAATGG	10523
Sbjct	10430	10489
Query	10524	ATACTTaaaaaaaTAAGGTTTCAAGGAAACCTCAACACCAAGAAAATGCTCAACCCAGGG	10583
Sbjct	10490T...	10549
Query	10584	AAACTATCTGAACAGTTGGACAGGGAGGGGCGCAAGAGGAACATCTACAACCACCAGATT	10643
Sbjct	10550	10609
Query	10644	GGTACTATAATGTCAAGTGCAGGCATAAGGCTGGAGAAATTGCCAATAGTGAGGGCCCAA	10703
Sbjct	10610	10669
Query	10704	ACCGACACCAAAACCTTTTCATGAGGCAATAAGAGATAAGATAGACAAGAGTGAAAACCGG	10763
Sbjct	10670	10729
Query	10764	CAAATCCAGAATTGCACAACAAATTGTTGGAGATTTTCCACACGATAGCCCAACCCACC	10823
Sbjct	10730	10789
Query	10824	CTGAAACACACCTACGGTGAGGTGACGTGGGAGCAACTTGAGGCGGGGTAAATAGAAAG	10883
Sbjct	10790A.....	10849
Query	10884	GGGGCAGCAGGCTTCCTGGAGAAGAAGAACATCGGAGAAGTATTGGATTTCAGAAAAGCAC	10943
Sbjct	10850	10909
Query	10944	CTGGTAGAACAATTGGTCAGGGATCTGAAGGCCGGGAGAAAGATAAAATATTATGAAACT	11003
Sbjct	10910	10969
Query	11004	GCAATACCAAAAAATGAGAAGAGAGATGTCAGTGATGACTGGCAGGCAGGGGACCTGGTG	11063
Sbjct	10970	11029
Query	11064	GTTGAGAAGAGGCCAAGAGTTATCCAATACCCTGAAGCCAAGACAAGGCTAGCCATCACT	11123
Sbjct	11030	11089
Query	11124	AAGGTCATGTATAACTGGGTGAAACAGCAGCCCGTTGTGATTCCAGGATATGAAGGAAAG	11183
Sbjct	11090	11149
Query	11184	ACCCCTTGTTCACATCTTTGATAAAGTGAGAAAGGAATGGGACTCGTTCAATGAGCCA	11243
Sbjct	11150	11209
Query	11244	GTGGCCGTAAGTTTTGACACCAAAGCCTGGGACACTCAAGTGACTAGTAAGGATCTGCAA	11303
Sbjct	11210	11269
Query	11304	CTTATTGGAGAAATCCAGAAATATTACTATAAGAAGGAGTGGCACAAAGTTCATTGACACC	11363
Sbjct	11270	11329
Query	11364	ATCACCGACCACATGACAGAAGTACCAGTTATAACAGCAGATGGTGAAGTATATATAAGA	11423
Sbjct	11330	11389
Query	11424	AATGGGCAGAGAGGGAGCGGCCAGCCAGACACAAGTGCTGGCAACAGCATGTTAAATGTC	11483
Sbjct	11390	11449
Query	11484	CTGACAATGATGTACGGCTTCTGCGAAAGCACAGGGGTACCGTACAAGAGTTTCAACAGG	11543
Sbjct	11450C.....	11509

Query	11544	GTGGCAAGGATCCACGTCTGTGGGGATGATGGCTTCTTAATAACTGAAAAAGGGTTAGGG	11603
Sbjct	11510	11569
Query	11604	CTGAAATTTGCTAACAAAGGGATGCAGATTCTTCATGAAGCAGGCAAACCTCAGAAGATA	11663
Sbjct	11570	11629
Query	11664	ACGGAAGGGGAAAAGATGAAAGTTGCCTATAGATTTGAGGATATAGAGTTCTGTTCTCAT	11723
Sbjct	11630	11689
Query	11724	ACCCAGTCCCTGTTAGGTGGTCCGACAACACCAGTAGTCACATGGCCGGGAGAGACACC	11783
Sbjct	11690	11749
Query	11784	GCTGTGATACTATCAAAGATGGCAACAAGATTGGATTCAAGTGGAGAGAGGGGTACCACA	11843
Sbjct	11750T	11809
Query	11844	GCATATGAAAAAGCGGTAGCCTTCAGTTTCTTGCTGATGTATTCCTGGAACCCGCTTGTT	11903
Sbjct	11810	11869
Query	11904	AGGAGGATTTGCCTGTTGGTCCTTTTCGCAACAGCCAGAGACAGACCCATCAAAACATGCC	11963
Sbjct	11870	11929
Query	11964	ACTTATTATTACAAAGGTGATCCAATAGGGGCCTATAAAGATGTAATAGGTCGGAATCTA	12023
Sbjct	11930	11989
Query	12024	AGTGAAGTGAAGAGAACAGGCTTTGAGAAATTGGCAAATCTAAACCTAAGCCTGTCCACG	12083
Sbjct	11990	12049
Query	12084	TTGGGGGTCTGGACTAAGCACACAAGCAAAAGAATAATTCAGGACTGTGTTGCCATTGGG	12143
Sbjct	12050A.....	12109
Query	12144	AAAGAAGAGGGCAACTGGCTAGTTAA-GCCCGACAGGCTGATATCCAGCAAACTGGCCA	12202
Sbjct	12110C...-.....	12168
Query	12203	CTTATACATACCTGATAAAGGCTTTACATTACAAGGAAAGCATTATGAGCAACTGCAGCT	12262
Sbjct	12169	12228
Query	12263	AAGAACAGAGACAAACCCGGTCATGGGG-TTGGGACTGAGAGATACAAGTTAGGTCCCAT	12321
Sbjct	12229G.....	12288
Query	12322	AGTCAATCTGCTGCTGAGAAGGTTGAAAATTCTGCTCATGACGGCCGTCGGCGTCAGCAG	12381
Sbjct	12289	12348
Query	12382	CTGAGACAAAATGTATATATTGTAAATAAATTAATCCATGTACATAGTGTATATAAATAT	12441
Sbjct	12349	12408
Query	12442	AGTTGGGACCGTCCACCTCAAGAAGACGACACGCCCAACACGCACAGCTAAACAGTAGTC	12501
Sbjct	12409	12468
Query	12502	AAGATTATCTACCTCAAGATAAACTACATTTAATGCACACAGCACTTTAGCTGTATGAG	12561
Sbjct	12469	12528
Query	12562	GATACGCCCCGACGTCTATAGTTGGACTAGGGAAGACCTCTAACAGCCCCC	12611
Sbjct	12529	12578

Score = 1284 bits (695), Expect = 0.0
 Identities = 695/695 (100%), Gaps = 0/695 (0%)
 Strand=Plus/Plus

Query	1	GTATACGAGAATTAGAAAAGGCACTCGTATACGTATTGGGCAATTAAAAATAATAATTAG	60
Sbjct	1	60
Query	61	GCCTAGGGAACAAATCCCTCTCAGCGAAGGCCGAAAAGAGGCTAGCCATGCCCTTAGTAG	120
Sbjct	61	120

Query	121	GACTAGCATAATGAGGGGGGTAGCAACAGTGGTGAGTTCGTTGGATGGCTTAAGCCCTGA	180
Sbjct	121	180
Query	181	GTACAGGGTAGTCGTCAGTGGTTCGACGCCTTGAATAAAGGTCTCGAGATGCCACGTGG	240
Sbjct	181	240
Query	241	ACGAGGGCATGCCCAAAGCACATCTTAACCTGAGCGGGGTCGCCCAGGTAAAAGCAGTT	300
Sbjct	241	300
Query	301	TTAACCGACTGTTACGAATACAGCCTGATAGGGTGCTGCAGAGGCCCACTGTATTGCTAC	360
Sbjct	301	360
Query	361	TAAAAATCTCTGCTGTACATGGCACATGGAGTTGATCACAAATGAACTTTTATACAAAAC	420
Sbjct	361	420
Query	421	ATACAAACAAAACCCGTCGGGGTGGAGGAACCTGTTTATGATCAGGCAGGTGATCCCTT	480
Sbjct	421	480
Query	481	ATTTGGTGAAAGGGGAGCAGTCCACCCTCAATCGACGCTAAAGCTCCACACAAGAGAGG	540
Sbjct	481	540
Query	541	GGAACGCGATGTTCCAACCAACTTGGCATCCTTACCAAAAAGAGGTGACTGCAGGTCGGG	600
Sbjct	541	600
Query	601	TAATAGCAGAGGACCTGTGAGCGGGATCTACCTGAAGCCAGGGCCACTATTTTACCAGGA	660
Sbjct	601	660
Query	661	CTATAAAGGTCCCGTCTATCACAGGGCCCCGCTGG	695
Sbjct	661	695

> [gi|9049956|gb|AF268278.1|AF268278](#) **D** Pestivirus type 1, complete genome
Length=12734

Score = 2.131e+04 bits (11537), Expect = 0.0
Identities = 11657/11691 (99%), Gaps = 8/11691 (0%)
Strand=Plus/Plus

Query	928	TTCAGACACGAAAGAAGAGGGAGCAACAAAAAAGAAAACACAGAAACCCGACAGACTAGA	987
Sbjct	1045	1104
Query	988	AAGGGGGAAAATGAAAATAGTGCCCAAAGAATCTGAAAAGACAGCAAACTAAACCTCC	1047
Sbjct	1105C..	1164
Query	1048	GGATGCTACAATAGTGGTGGAGGAGTCAAATACCAGGTGAGGAAGAAGGGAAAAACCAA	1107
Sbjct	1165	1224
Query	1108	GAGTAAAAACACTCAGGACGGCTTGTACCATAACAAAAACAAACCTCAGGAATCAGCAA	1167
Sbjct	1225	1284
Query	1168	GAAACTGGAAAAAGCATTGTTGGCGTGGGCAATAATAGCTATAGTTTTGTTTCAAGTTAC	1227
Sbjct	1285C.....	1344
Query	1228	AATGGGAGAAAACATAACACAGTGGAACCTACAAGATAATGGGACGGAAGGGATACAACG	1287
Sbjct	1345	1404
Query	1288	GGCAATGTTCCAAAGGGGTGTGAATAGAAGTTTACATGGAATCTGGCCAGAGAAAATCTG	1347
Sbjct	1405	1464
Query	1348	TACTGGCGTCCCTTCCCATCTAGCCACCGATATAGAACTAAAAACAATTCATGGTATGAT	1407
Sbjct	1465T.....	1524
Query	1408	GGATGCAAGTGAGAAGACCAACTACACGTGTTGCAGACTTCAACGCCATGAGTGGAACAA	1467
Sbjct	1525A.....	1584

Query	1468	GCATGGTTGGTGCAACTGGTACAATATTGAACCCTGGATTCTAGTCATGAATAGAACCCA	1527
Sbjct	1585	1644
Query	1528	AGCCAATCTCACTGAGGGACAACCACCAAGGGAGTGCGCAGTCACTTGTAGGTATGATAG	1587
Sbjct	1645	1704
Query	1588	GGCTAGTGACTTAAACGTGGTAACACAAGCTAGAGATAGCCCCACACCCTTAACAGGTTG	1647
Sbjct	1705	1764
Query	1648	CAAGAAAGGAAAGAACTTCTCCTTTGCAGGCATATTGATGCGGGGCCCTGCAACTTTGA	1707
Sbjct	1765	1824
Query	1708	AATAGCTGCAAGTGATGTATTATTCAAAGAACATGAACGCATTAGTATGTTCCAGGATAC	1767
Sbjct	1825	1884
Query	1768	TACTCTTTACCTTGTTGACGGGTTGACCAACTCCTTAGAAGGTGCCAGACAAGGAACCGC	1827
Sbjct	1885	1944
Query	1828	TAAACTGACAACCTGGTTAGGCAAGCAGCTCGGGATACTAGGAAAAAAGTTGGAAAAACA	1887
Sbjct	1945	2004
Query	1888	GAGTAAGACGTGGTTTGGAGCATACGCTGCTTCCCCTTACTGTGATGTGCGATCGCAAAT	1947
Sbjct	2005T.....	2064
Query	1948	TGGCTACATATGGTATACAAAAATTGCACCCCTGCCTGCTTACCCAAGAACACAAAAAT	2007
Sbjct	2065	2124
Query	2008	TGTCGGCCCTGGGAAATTTGACACCAATGCAGAGGACGGCA-GATATTACATGAGATGGG	2066
Sbjct	2125A.....	2184
Query	2067	GGGTCACCTTGTCGGAGGTACTACTACTTTCTTTAGTGGTGCTGTCCGACTTCGCACCGGA	2126
Sbjct	2185	2244
Query	2127	AACAGCTAGTGTAATGTACCTAATCCTACATTTTTCCATCCCACAAAGTCACGTTGATGT	2186
Sbjct	2245	2304
Query	2187	AATGGATTGTGATAAGACCCAGTTGAACCTCACAGTGGAGCTGACAACAGCTGAAGTAAT	2246
Sbjct	2305T.....	2364
Query	2247	ACCAGGGTCGGTCTGGAATCTAGGCAAATATGTATGTATAAGACCAAATTGGTGGCCTTA	2306
Sbjct	2365	...T..A..A.....C.....GG.....	2424
Query	2307	TGAGACAACCTGTAGTGTTGGCATTGGAAGAGGTGAGCCAGGTGGTGAAGTTAGTGTTGAG	2366
Sbjct	2425G.....	2484
Query	2367	GGCACTCAGAGATTTAACACGCATTTGGAACGCTGCAACAACACTACTGCTTTTTTAGTATG	2426
Sbjct	2485G.....C...A....	2544
Query	2427	CCTTGTTAAGATAGTCAGGGGCCAGATGGTACAGGGCATTCTGTGGCTACTATTGATAAC	2486
Sbjct	2545C.....	2604
Query	2487	AGGGGTACAAGGGCACTTGGATTGCAAACCTGAATTCTCGTATGCCATAGCAAAGGACGA	2546
Sbjct	2605	2664
Query	2547	AAGAATTGGTCAACTGGGGGCTGAAGGCCTTACCACCACTTGAAGGAATACTCACCTGG	2606
Sbjct	2665	2724
Query	2607	AATGAAGCTGGAAGACACAATGGTCATTGCTTGGTGCGAAGATGGGAAGTTAATGTACCT	2666
Sbjct	2725	2784
Query	2667	CCAAAGATGCACGAGAGAAACCAGATATCTCGCAATCTTGCATACAAGAGCCTTGCCGAC	2726
Sbjct	2785	2844
Query	2727	CAGTGTGGTATTCAAAAACTCTTTGATGGGCGAAAGCAAGAGGATGTAGTCGAAATGAA	2786
Sbjct	2845	2904

Query	2787	CGACAACCTTTGAATTTGGACTCTGCCCATGTGATGCCAAACCCATAGTAAGAGGGAAGTT	2846
Sbjct	2905	2964
Query	2847	CAATACAACGCTGCTGAACGGACCGGCCTTCCAGATGGTATGCCCCATAGGATGGACAGG	2906
Sbjct	2965	3024
Query	2907	GACTGTAAGCTGTACGTCATTCAATATGGACACCTTAGCCACAACCTGTGGTACGGACATA	2966
Sbjct	3025	3084
Query	2967	TAGAAGGTCTAAACCATTCCCTCATAGGCAAGGCTGTATCACCCAAAAGAATCTGGGGGA	3026
Sbjct	3085	3144
Query	3027	GGATCTCCATAAAGTGCATCCTTGGAGGAAATTGGACTTGTGTGCCTGGAGACCAACTACT	3086
Sbjct	3145	3204
Query	3087	ATACAAAGGGGGCTCTATTGAATCTTGCAAGTGGTGTGGCTATCAATTTAAAGAGAGTGA	3146
Sbjct	3205	3264
Query	3147	GGGACTACCACACTACCCCATTTGGCAAGTGTAATTGGAGAACGAGACTGGTTACAGGCT	3206
Sbjct	3265	3324
Query	3207	AGTAGACAGTACCTCTTGCAATAGAGAAGGTGTGGCCATAGTACCACAAGGGACATTAAA	3266
Sbjct	3325	3384
Query	3267	GTGCAAGATAGGAAAAACAACCTGTACAGGTCATAGCTATGGATACCAAACCTCGGACCTAT	3326
Sbjct	3385	3444
Query	3327	GCCTTGCAGACCATATGAAATCATATCAAGTGAGGGGCCTGTAGAAAAGACAGCGTGTAC	3386
Sbjct	3445	3504
Query	3387	TTTCAACTACACTAAGACATTAAAAAATAAGTATTTTGAGCCCAGAGACAGCTACTTTCA	3446
Sbjct	3505	3564
Query	3447	GCAATACATGCTAAAAGGAGAGTATCAATACTGGTTTGACCTGGAGGTGACTGACCATCA	3506
Sbjct	3565	3624
Query	3507	CCGGGATTACTTCGCTGAGTCCATATTAGTGGTGGTAGTAGCCCTCTTGGGTGGCAGATA	3566
Sbjct	3625	3684
Query	3567	TGTACTTTGGTTACTGGTTACATACATGGTCTTATCAGAACAGAAGGCCTTAGGGATTCA	3626
Sbjct	3685	3744
Query	3627	GTATGGATCAGGGGAAGTGGTGATGATGGGCAACTTGCTAACCATAACAATATTGAAGT	3686
Sbjct	3745	3804
Query	3687	GGTGACATACTTCTTGCTGCTGTACCTACTGCTGAGGGAGGAGAGCGTAAAGAAGTGGGT	3746
Sbjct	3805	3864
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 Identities = 405/406 (99%), Gaps = 0/406 (0%)
 Strand=Plus/Plus

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#6 Search #5 AND (Npro or autoprotease) Field: Title/Abstract	15:18:06	10
#5 Related Articles for PubMed (Select 9499097)	15:17:44	284
#4 Search (Npro or autoprotease) AND ("bovine viral diarrhea" or BVDV*) AND (inactiv* or truncat* or modif* or muta* or delet*) Field: Title/Abstract	15:17:39	7
#2 Search (Npro or autoprotease) AND ("bovine viral diarrhea" or BVDV*) AND (inactiv* or truncat* or modif* or muta*) Field: Title/Abstract	15:16:32	6

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Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L5	L4 and Npro	4
<input type="checkbox"/>	L4	((bvd or bovine adj viral adj diarrhe\$5) adj virus or BVDV) same (Npro or protease or autoprotease) same attenuat\$8	11
<input type="checkbox"/>	L3	((bvd or bovine adj viral adj diarrhe\$5) adj virus or BVDV) same (Npro or autoprotease) and (Npro or autoprotease or protease or proteinase)with (attenuat\$5 or modif\$8 or muta\$5 or delet\$5 or substitut\$6)	14
<input type="checkbox"/>	L2	((bvd or bovine adj viral adj diarrhe\$5) adj virus or BVDV) same (Npro or autoprotease) same (attenuat\$5 or modif\$8 or muta\$5 or delet\$5 or substitut\$6)	6
<input type="checkbox"/>	L1	((bvd or bovine adj viral adj diarrhe\$5) adj virus or BVDV) same (Npro or autoprotease) same (attenuat\$5 or modif\$8 or muta\$5 or delet\$5)	6

END OF SEARCH HISTORY